

CLAIMS:

1. An isolated nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding an amino acid sequence having homology to a regulator of gene expression or a derivative of said gene regulator.
2. An isolated nucleic acid molecule according to claim 1 wherein the regulator comprises a zinc finger domain of an $(\text{HC}_3)_2$ type.
3. An isolated nucleic acid molecule according to claim 2 wherein the sequence of nucleotides or complementary sequence of nucleotides is selected from:
 - (i) a nucleotide sequence set forth in SEQ ID NO:2;
 - (ii) a nucleotide sequence encoding an amino acid sequence set forth in SEQ ID NO:3;
 - (iii) a nucleotide sequence having at least about 40% similarity to the nucleotide sequence of (i) or (ii); and
 - (iv) a nucleotide sequence capable of hybridising under low stringency conditions to the nucleotide sequence set forth in (i), (ii) or (iii).
4. An isolated nucleic acid molecule according to claim 1 wherein said gene regulator is a guanine nucleotide exchange factor (GEF) or a derivative thereof.
5. An isolated nucleic acid molecule according to claim 4 wherein the sequence of nucleotides is selected from:
 - (i) a nucleotide sequence set forth in SEQ ID NO:4 or 6;
 - (ii) a nucleotide sequence encoding an amino acid sequence set forth in SEQ ID NO:5 or 7;
 - (iii) a nucleotide sequence having at least about 40% similarity to the nucleotide sequence of (i) or (ii); and
 - (iv) a nucleotide sequence capable of hybridising under low stringency conditions to the

nucleotide sequence set forth in (i), (ii) r (iii).

6. An isolated nucleic acid molecule according to claim 1, wherein said gene regulator is a heat shock protein or is a heat shock binding protein or a derivative thereof.

7. An isolated nucleic acid molecule according to claim 6, wherein the sequence of nucleotides is selected from:

- (i) a nucleotide sequence set forth in SEQ ID NO:8;
- (ii) a nucleotide sequence encoding an amino acid sequence set forth in SEQ ID NO:9;
- (iii) a nucleotide sequence having at least about 40% similarity to the nucleotide sequence of (i) or (ii); and
- (iv) a nucleotide sequence capable of hybridising under low stringency conditions to the nucleotide sequence set forth in (i), (ii) or (iii).

8. A genetic construct comprising a vector portion and a gene portion comprising a regulator of gene expression or a derivative thereof.

9. A genetic construct according to claim 8 wherein the gene portion comprises a zinc finger domain of $(\text{HC}_3)_2$ type.

10. A genetic construct according to claim 9 wherein the gene portion comprises a nucleotide sequence selected from:

- (i) a nucleotide sequence set forth in SEQ ID NO:2;
- (ii) a nucleotide sequence encoding an amino acid sequence set forth in SEQ ID NO:3;
- (iii) a nucleotide sequence having at least about 40% similarity to the nucleotide sequence of (i) or (ii); and
- (iv) a nucleotide sequence capable of hybridising under low stringency conditions to the nucleotide sequence set forth in (i), (ii) or (iii).

11. A genetic construct according to claim 8 wherein said gene portion is a nucleotide exchange factor (GEF) or derivative thereof.
12. A genetic construct according to claim 11 wherein the gene portion comprises a nucleotide sequence selected from:
- (i) a nucleotide sequence set forth in SEQ ID NO:4 or 6;
 - (ii) a nucleotide sequence encoding an amino acid sequence set forth in SEQ ID NO:5 or 7;
 - (iii) a nucleotide sequence having at least about 40% similarity to the nucleotide sequence of (i) or (ii); and
 - (iv) a nucleotide sequence capable of hybridising under low stringency conditions to the nucleotide sequence set forth in (i), (ii) or (iii).
13. A genetic construct according to claim 8 wherein the gene portion is a heat shock protein or a derivative thereof or a heat shock binding protein or derivative thereof.
14. A genetic construct according to claim 13 wherein the gene portion comprises a nucleotide sequence selected from:
- (i) a nucleotide sequence set forth in SEQ ID NO:8;
 - (ii) a nucleotide sequence encoding an amino acid sequence set forth in SEQ ID NO:9;
 - (iii) a nucleotide sequence having at least about 40% similarity to the nucleotide sequence of (i) or (ii); and
 - (iv) a nucleotide sequence capable of hybridising under low stringency conditions to the nucleotide sequence set forth in (i), (ii) or (iii).
15. A nucleic acid molecule encoding a gene regulator having the identifying characteristics of a molecule selected from MCG4, MCG7 and MCG18 having respective amino acid sequences of SEQ ID NO:3, SEQ ID NO: 5 or 7 and SEQ ID NO:9.

16. A method of detecting a condition caused or facilitated by an aberration in *mcg4*, said method comprising determining the presence of a single or multiple nucleotide substitution, deletion and/or addition or other aberration to one or both alleles of said *mcg4* wherein the presence of such a nucleotide substitution, deletion and/or addition or other aberration may be indicative of said condition or a propensity to develop said condition.
17. A method of detecting a condition caused or facilitated by an aberration in *mcg4*, said method comprising screening for a single or multiple amino acid substitution, deletion and/or addition to MCG4 wherein the presence of such a mutation is indicative of or a propensity to develop said condition.
18. A method for detecting MCG4 or a derivative thereof in a biological sample said method comprising contacting said biological sample with an antibody specific for MCG4 or its derivatives or homologues for a time and under conditions sufficient for an antibody-MCG4 complex to form, and then detecting said complex.
19. A method of detecting a condition caused or facilitated by an aberration in *mcg7*, said method comprising determining the presence of a single or multiple nucleotide substitution, deletion and/or addition or other aberration to one or both alleles of said *mcg7* wherein the presence of such a nucleotide substitution, deletion and/or addition or other aberration may be indicative of said condition or a propensity to develop said condition.
20. A method of detecting a condition caused or facilitated by an aberration in *mcg7*, said method comprising screening for a single or multiple amino acid substitution, deletion and/or addition to MCG7 wherein the presence of such a mutation is indicative of or a propensity to develop said condition.
21. A method for detecting MCG7 or a derivative thereof in a biological sample said method comprising contacting said biological sample with an antibody specific for MCG7 or its derivatives or homologues for a time and under conditions sufficient for an antibody-MCG7 complex to form, and then detecting said complex.

22. A method of detecting a condition caused or facilitated by an aberration in *mcg18*, said method comprising determining the presence of a single or multiple nucleotide substitution, deletion and/or addition or other aberration to one or both alleles of said *mcg18* wherein the presence of such a nucleotide substitution, deletion and/or addition or other aberration may be indicative of said condition or a propensity to develop said condition.

23. A method of detecting a condition caused or facilitated by an aberration in *mcg18*, said method comprising screening for a single or multiple amino acid substitution, deletion and/or addition to MCG18 wherein the presence of such a mutation is indicative of or a propensity to develop said condition.

24. A method for detecting MCG18 or a derivative thereof in a biological sample said method comprising contacting said biological sample with an antibody specific for MCG18 or its derivatives or homologues for a time and under conditions sufficient for an antibody-MCG18 complex to form, and then detecting said complex.

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